

SCORE Search Results Details for Application 10578781 and Search Result 20081104_154455_us-10-578-1

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This page gives you Search Results detail for the Application 10578781 and Search Result 20081104_154455_us-10-578-1

GenCore version 6.3
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QM nucleic - nucleic search, using sw model

Run on: November 4, 2008, 17:10:38 ; Search time 1527 Seconds
(without alignments)
45700.779 Million cell updates/sec

Title: US-10-578-781-1
Perfect score: 756
Sequence: 1 at gggg gccgat at caaaaa.....aggagcaaat t gaacatt ag 756

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 11299264 seqs, 46154159321 residues

Total number of hits satisfying chosen parameters: 22598528

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEntbl: *
1: gb_env: *
2: gb_pat: *
3: gb_ph: *
4: gb_pl: *
5: gb_pr: *
6: gb_ro: *
7: gb_sts: *
8: gb_sy: *
9: gb_un: *
10: gb_vi: *
11: gb_ov: *
12: gb_in: *
13: gb_om: *
14: gb_ba: *
15: gb_ht g1: *
16: gb_ht g2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	% Query Match	Length	DB ID	Description
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1	756	100.0	756	2	DD160143	DD160143 Novel Bre
2	756	100.0	756	2	DI 115290	DI 115290 Novel Bre
3	366.2	48.4	1746	14	BACSPQI	L47358 Paeni bacilli
4	363.2	48.0	1799	14	Z54161	Z54161 B. coagulans
5	361.6	47.8	3701	14	AJ704768	AJ704768 Bacillus
c 6	361.6	47.8	110000	14	CP000560_22	Continuation (23 o
c 7	354.6	46.9	110000	14	CP000813_21	Continuation (22 o
c 8	353.6	46.8	110000	14	CP000557_23	Continuation (24 o
9	348.4	46.1	110000	14	AP006627_19	Continuation (20 o
10	345.6	45.7	864	14	BACSPQ2A	M15744 B. subtilis
c 11	345.6	45.7	204537	14	Z99116	Z99116 Bacillus su
12	345.6	45.7	282700	14	BACJH642	D84432 Bacillus su
13	343	45.4	110000	14	BA000004_16	Continuation (17 o
c 14	342	45.2	110000	14	CP000764_28	Continuation (29 o
15	339.6	44.9	1920	14	X63757	X63757 B. megateriu
c 16	338.8	44.8	110000	14	AE016877_40	Continuation (41 o
c 17	338.2	44.7	110000	14	AE017194_38	Continuation (39 o
c 18	333.8	44.2	110000	14	BA000043_23	Continuation (24 o
c 19	333.4	44.1	110000	14	CP000903_39	Continuation (40 o
c 20	330.2	43.7	110000	14	CP000001_39	Continuation (40 o
c 21	330.2	43.7	110000	14	CP000485_39	Continuation (40 o
c 22	330.2	43.7	110000	14	AE016879_39	Continuation (40 o
c 23	330.2	43.7	110000	14	AE017225_39	Continuation (40 o
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c 26	330.2	43.7	110000	14	AE017355_39	Continuation (40 o
27	329.4	43.6	1777	14	BACSPQI B	L47360 Bacillus st
28	328.6	43.5	759	8	EF039064	EF039064 Syntheti
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c 43	231	30.6	110000	14	CP000930_04	Continuation (5 o
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c 45	223.6	29.6	110000	14	CP000930_20	Continuation (21 o

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION Novel Brevibacillus choshinensis and Producing Method of Protein by Using Theroplas Host.
 ACCESSION DD160143
 VERSION DD160143.1 GI: 83960018
 KEYWORDS WD 2005045005-A.1.
 SOURCE Brevibacillus choshinensis
 ORGANISM Bacteria; Firmicutes; Bacillales; Paeni bacillaceae; Brevibacillus.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS Hanagata, H. and Nishijyo, T.
 TITLE Novel Brevibacillus choshinensis and Producing Method of Protein by Using Theroplas Host
 JOURNAL Patent: WO 2005045005-A 1 19-MAY-2005;
 Hgeta Shoyu Co Ltd
 COMMENT CS Brevibacillus choshinensis

PN WO 2005045005- A/ 1
 PD 19- MAY- 2005
 PF 08- NOV- 2004 WO 2004JP016912
 PR 11- NOV- 2003 JP 03P 381606
 PI hi roshi hanagat a, takayuki ni shi j yo
 OC
 FH Key Location/ Qual if i e r s.

FEATURES
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 /db _xref ="taxon: 54911"

ORI G N

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 Best Local Si milarity 100.0% Pred. Nb. 6.7e-232;
 Matches 756; Conser vative 0; M smatches 0; Indels 0; Gaps 0;

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Db	121	ATCAGACTGGTCTGGTCCGTGGTCCAGGCTTTATCAACGGGGATATGAAGGGGATGAT	180
Qy	181	TTGTTTCAGATGGGTTGCATTGGCTTGCTCAAGGGGGTTGACAAGTTGGATCTTTGGTAC	240
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Qy	241	GATGTGAGATTTTGGACCTATGGGTGCAATGATCATGGGAGAAATTCAGGCTTTTGG	300
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Db	601	AGGCTGAGGGAGGGTGAAGGCTCATGGTCTAAGTGGGCTATTACAAGGATCAGACACAG	660
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Db      601  AGGCTGAGGAGCGGTGAGCAGCTCATCGTCTACCTGCCTATTACAAGGATCAGACACAG 660
Qy      661  TCTGAGGTAGCAGAGCGGTCTAGGGATTTCG CAGGTCAGGTCCTCGGCTCTGGAAAAGGGT 720
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Db      721  ATCTGCTAACGATCAAGGAGCAAATTGAACATTAG 756

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RESULT 3

BACSPQI

LOCUS BACSPQI 1746 bp DNA linear BCT 16- CCT- 1997
 DEFINITION Paenibacillus polymyxa spoliAA, spoliAB, and sigma factor genes,
 complete cds.

ACCESSION

L47358

VERSION

L47358.1 GI:2529264

KEYWORDS

SOURCE

Paenibacillus polymyxa

ORGANISM

Paenibacillus polymyxa

REFERENCE

Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.

AUTHORS

1 (bases 1 to 1746);
 Park, S. G. and Yudkin, M. D.

TITLE

Sequencing and phylogenetic analysis of the spoliA operon from

JOURNAL

di verse Bacillus and Paenibacillus species

PUBMED

Gene 194 (1), 25-33 (1997)

COMMENT

9266669

FEATURES

OSDB: S:46599.

source
 Location/Qualifiers
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-35_signal

6..11

/inference="non-experimental evidence, no additional
 details recorded"

-10_signal

29..33

/inference="non-experimental evidence, no additional
 details recorded"

gene

70..423

/gene="spoliAA"

CDS

70..423

/gene="spoliAA"

/inference="non-experimental evidence, no additional
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/translation="1"

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/db_xref="GI:2529265"

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HIVLSLKNLQFMDSGLGVI LGRYKLI NQKGGEMAVCDVNPVHRLLDVMSGLFKI MPI

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CDS

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CDS

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TSI HETVFENDGDI TLMDQI ADESOERWFDKALNEAI DGLSERERLI VYLRYRDIQ
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ORIGIN

Query Match 48.4% Score 366.2; DB 14; Length 1746;
 Best Local Similarity 67.8% Pred. No. 5.2e-106;
 Matches 512; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

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Qy      1  ATGGGTGGCGATATCAAAAATGGAGTCAACCAATTTCTGAACCAATGACCAAGTGAAGAAAT 60
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Qy      61  TTGATAGCCAAAGAGCCAAAGCTGGCGATAAGCATGCAAGTCTCTGGTGAATAGCAAT 120
Db      947  CTTATGCACTGAGTCAATCTGGTGATAATGATGCTGGTGAGACACTAATCAATAGTAAT 1006
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Db     1007  ATGGGCTGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1066
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Qy     481  TCTCCATCCATGAGAGCGTTTTTGAAGATGAAGGGATCCATCACACTGATGATCAG 540
Db     1367  ACGTCCATTCAGGAACAGTGTGTGAAGATGAAGGAGAGGAGGATACACTATGATGATCAG 1426
Qy     541  ATAGCGGATGAAGGTTGAACAAGTGGTTTGAAGAAATTTGGCTTGAAGGAGGAGGAGGAGG 600
Db     1427  ATTGGGAGGAGATGGAGGAGGAGGAGTGGTGGAGAGGCTGGGGTGAATGAGGGCAATTGAC 1486
Qy     601  AGGCTGAGGGAGGCTGAGCAGCTCATGGTCTAAGTGGGCTATTACAAGGATCAGACACAG 660
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Qy 661 TCTGAGGTACGAGCGCTTAGCGATTGCGAGGTCCAGGTCTCGGGTCTGGAAAAGCGT 720
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 Qy 721 ATCTGCTAACGATCAAGGAGCAAAATTGAACATTA 755
 Db 1607 ATTTTACAACAGATCGCGATCAGATTGCCAATA 1641

RESULT 4

Z54161
 LOCUS Z54161 1799 bp DNA linear BCT 18-APR-2005
 DEFINITION B.coagulans genes for SpoIIAA, SpoIIAB and sigma factor.
 ACCESSION Z54161
 VERSION Z54161.1 G:1552541
 KEYWORDS sigma factor; SpoIIAA; SpoIIAB.
 SOURCE Bacillus coagulans
 ORGANISM Bacillus coagulans
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (bases 1 to 1799)
 AUTHORS Park, S.G. and Yudkin, M.D.
 TITLE Nucleotide sequence of the Bacillus coagulans homologue of the spoIIA operon of Bacillus subtilis
 JOURNAL Gene 177 (1-2), 275-276 (1996)
 PUBMED 8921882
 REFERENCE 2 (bases 1 to 1799)
 AUTHORS Park, S.S.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-1995) Sung Goo SG Park, Microbiology Unit, Biochemistry, University of Oxford, South Parks Road, Oxford, OX1 3QU, UK

FEATURES
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Query Match 48.0% Score 363.2; DB 14; Length 1799;
Best Local Similarity 69.4% Pred. No. 4.9e-105;
Matches 494; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

<http://es/ScoreAccessWeb/GetItem.action?AppId=10578781&seqId=09323b67809> 11/6/08

Db 1650 CACGGCTTGAAAGAAATACCTTCAGTGATGAAAGAGCGCATGGAATTGTA 1701

RESULT 5
 AJ704768
 LOCUS 3701 bp DNA linear BCT 10-MAY-2005
 DEFINITION *Bacillus anlyoliquefaciens* dacF gene, spoIIA operon and spoVAA gene (partial), strain FZB42.
 ACCESSION AJ704768
 VERSION 1
 KEYWORDS anti-sigma F factor antagonist; anti-sigmaF factor; dacF gene; penicillin binding protein; sigF gene; Sigma F; spoIIA gene; spoIIAB gene; spoVAA gene; Stage V sporulation protein AA.
 SOURCE *Bacillus anlyoliquefaciens* FZB42
 ORGANISM *Bacillus anlyoliquefaciens* FZB42
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 REFERENCE 1
 AUTHORS Stragier, P.
 TITLE Comparison of early sporulation genes in *Bacilli* and *Clostridia*
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3701)
 AUTHORS Borriess, R.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAY-2004) Borriess R., Biology, Humboldt University, Chaussee Strasse 117, D-10115, GERMANY
 COMMENT spoIIA operon 1290 - 3083.
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 IFLERGEEMIVKEMKGI ALASNDASVAMAEYI AGSEEDFVSFNNKKAKELGLKDS
 FKNPITGLPEKDIYSSAYDNKKMAKELLKYDKI TQFTGTEDYLRNTDKFVWNTNR
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/protein_id="CAG28934.1"
/db_xref="GI:63146683"

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/ db_xref="UniProt KB/ TrEMBL: Q50J80"
 / translation="MERRI FLRLRHRVKAHTGDIITIGDAAQ AGQCKLKKLSALPL
 YKVTKKDKNI VVLDI I KVLKTI HTAFPALDVOTVGGAEI VET HYQKQL SAVL FVG/
 WLLFI GSCLAI MNFHEVDSMREVHI ALYEI I TGERNEYPLLQI PYSI GLGLGM VF
 FNHI FKRLR.NEESPSPLEVMFNQLDLDRVAMHENEETMKDLHR"

ORIGIN

Query Match 47.8% Score 361.6; DB 14; Length 3701;
 Best Local Similarity 67.9% Pred. No. 1.8e-104;
 Matches 505; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

Qy 10 GATATCAAAAATGGGAGTCAACGATTTCTGACCAATGAOCAAAGTGAAGATTTGATAGCC 69
 Db 2202 GTTAAGAAAAACGAAAAACGGGACGCTCAAGGACCATGAAGTCAAAGATTAATCAAA 2261
 Qy 70 AAGAGCCAAAGCTGGGATACGGATGCAAGTGAAGTCTCTGTAATAGCAATATCAGACTG 129
 Db 2262 AAGAGCCAAAGGAGGACGACGAGGCAAGGAGAGCTCTCATAGAAAAAATCATGGCTCTT 2321
 Qy 130 GTCTGGTGGTGGTGGTGGGCTTTTATCAACGGGGGATGAAGGGGATGATTTGTTTCAG 189
 Db 2322 GTGTGGTGGTGGTGGTGGGCTTTTAAACAGAGGCTATGAGGGGATGATCTGTTTCAG 2381
 Qy 190 ATGGGTTGCATTGGCTTGGTCAAGGGGCTTGACAAGTGGATCTTGGTACGATGTGAGA 249
 Db 2382 ATGGGCTGTATGGGATTTGTTAAATGGTGTATAAATGGATTTGTCTATGATGTGGT 2441
 Qy 250 TTTTCAACCTATGGGGTGGCAATGATCATGCGAGAAATCAAGCGCTTTTGGGGATGAC 309
 Db 2442 TTTTCAACTTATGGGGTGGGATGATTTATGCGAGAAATCGAGGGTTCATCGGGATGAC 2501
 Qy 310 GGTACGGTTAAGGTGAGTGGATGGTTAAAAAGAAACAGGAAATGAAGTGGGGATCAAG 369
 Db 2502 GGAACGGTCAAAGTTTCAAGATCTTTAAAGAGCTGGGCAATAAAAAGCGGGGGAAA 2561
 Qy 370 GATGAATTTGTACAAGCAATGGGGTGGGGCAAGATGGGAGAGTGGGAGAGCAGTG 429
 Db 2562 GATGAAGTGTCAAAAAACATAGGAGAGTGGGGAGGGTGGGAGAAATGGGAGCAACATTTA 2621
 Qy 430 GGAATCAAGGGGAGGAGTGTCTTTGGGCAAGAGGCAAGGAGGAGGGCTTCTCCATC 489
 Db 2622 GAAATTTGATGGGAGGATGTGGTGGTGGGAGGAGGGGGTGGGGGGCTTCATGCAAT 2681
 Qy 490 CATGAGAGGGTTTTAAAAATGAGGGGATGGCATCACTGATGGATGAGATAGGGAT 549
 Db 2682 CATGAGAGGGTGTATGAAATGAGGAGAGGGGATCAAGCTGCTTGTGATGATAGGGAT 2741
 Qy 550 GAAGGTGTGAACAAGTGGTTTGAGAAAAATGGCTTGAAGGAGGGATCAGCAGGGCTGAGC 609
 Db 2742 CATTGAGAGAGAGAGTGGTTTGACAAAAATGGGGCTCAAGGAGGGGATCAGTGATTTGAG 2801
 Qy 610 GAGGGTGAAGAGCTCATGGTCTACCTGGGCTATTACAAGGATCAGACAGAGTCTGAGTA 669
 Db 2802 GAAGGGGAAAAAAGCTCATGTCTATCTGAGATATTATTAAGATCAGACAGAGTGGGAGTA 2861
 Qy 670 GCAGAGGGTCTAGGGATTTGGAGGTCAGGTCCTGGGCTCTGAAAAAGGGTATGCTGCTA 729
 Db 2862 GGGAGAGGGCTGGGATTTGGCAAGTCCAGGATGAGGGCTGGAGAAAAAATATTAAAG 2921
 Qy 730 ACGATCAAGGAGCAAAATTGAACAT 753
 Db 2922 CAGATTAAAGTGCAGATGGATCAT 2945

RESULT 6
 CP000560_22/c
 WPCOMMENT

Sequence split into 40 fragments LOCUS CP000560 Accession CP000560
 Fragment Name Begin End

Query Match 47.8% Score 361.6; DB 14; Length 110000;
Best Local Similarity 67.9% Pred. No. 3.1e-104;
Matches 505; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

<http://es/ScoreAccessWeb/GetItem.action?AppId=10578781&seqId=09323b67809...> 11/6/08

Qy 370 GATGAATTGTACAAGCAATTGGGCGTGGGCGAGATGCGAGAAAGTGCGCAAGCAGT 429

Db 46890 GATGAAGTGTCAAAAAACATACGGAAGAGTGCGGACCGTCCAGGAAATCGGGACCAATTTA 46831

Qy 430 GGAATCACGCGGAGGAGTAGTCTTTGGGCAAGAGGCAAGCAGAGGCGCTTCTCCATC 489

Db 46830 GAAATTGATGCGGAGGATGTGGTCTTGGGAGGAAAGCGTGCGGGCGCTTCATCCATT 46771

Qy 490 CATGAGACCGTTTTTGAAGATGACGGGATCCCATCACACTGATCGATCAGATAGCGGAT 549

Db 46770 CATGAGACCGTGTATGAAATGACGGAGACCGGATCACCTGCTTGTATCAGATGCGCGAT 46711

Qy 550 GAGGTGTGAACAAGTGGTTTGAGAAAAATTGCCTTGAAGGACGCGCATCAGCAGGCTGAGC 609

Db 46710 CATTGAGAAGAGAGTGGTTTGACAAAAATCGGCTCAAGGAGGCGATCAGTGATTTGGAA 46651

Qy 610 GAGGTGAGCAGCTCATCGTCTACCTGGGCTATTACAAGGATCAGACAGCTGAGGTA 669

Db 46650 GAAAGGAAAAACTCATTGTCTATCTGAGATATTATAAAGATCAGACAGTGGGAGTA 46591

Qy 670 GCAGAGCGTCTAGGGAATTTGGCAGGTCCAGGTCTGGGCTGCGAAAAAGGATCCTGCTA 729

Db 46590 GCGAAGCGCTGGGATTTTCCAAAGTCCAGGTATGAGGCTGGAGAAAAAATATTAAAG 46531

Qy 730 ACGATCAAGGAGCAAAATTGAACAT 753

Db 46530 CAGATTAAGTGCAGATGGATCAT 46507

RESULT 7

CP000813_21/c

WPCOMMENT

Sequence split into 37 fragments LOCUS CP000813 Accession CP000813

Fragment Name	Begin	End
CP000813_00	1	110000
CP000813_01	100001	210000
CP000813_02	200001	310000
CP000813_03	300001	410000
CP000813_04	400001	510000
CP000813_05	500001	610000
CP000813_06	600001	710000
CP000813_07	700001	810000
CP000813_08	800001	910000
CP000813_09	900001	1010000
CP000813_10	1000001	1110000
CP000813_11	1100001	1210000
CP000813_12	1200001	1310000
CP000813_13	1300001	1410000
CP000813_14	1400001	1510000
CP000813_15	1500001	1610000
CP000813_16	1600001	1710000
CP000813_17	1700001	1810000
CP000813_18	1800001	1910000
CP000813_19	1900001	2010000
CP000813_20	2000001	2110000
CP000813_21	2100001	2210000
CP000813_22	2200001	2310000
CP000813_23	2300001	2410000
CP000813_24	2400001	2510000
CP000813_25	2500001	2610000
CP000813_26	2600001	2710000
CP000813_27	2700001	2810000
CP000813_28	2800001	2910000
CP000813_29	2900001	3010000
CP000813_30	3000001	3110000
CP000813_31	3100001	3210000
CP000813_32	3200001	3310000
CP000813_33	3300001	3410000

CP000813_34 3400001 3510000
 CP000813_35 3500001 3610000
 CP000813_36 3600001 3704465

Continuation (22 of 37) of CP000813 from base 2100001 (CP000813 *Bacillus pumilus* SAFR-

Query Match 46.9% Score 354.6; DB 14; Length 110000;
 Best Local Similarity 67.6% Pred. No. 5.6e-102;
 Matches 498; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

```

Qy      16  AAAAATTGCGAGTCAACCATTTCTGACCAATGAACAGTGAAGATTGATAGGCAAGAGC 75
Db      14501 AAGCAAGCAAAAAAGGCCAGCTGTCAATGATGAAGTCAAGAGCTCATCAAAAAAGC 14442

Qy      76  CAAGCTGGGATACGGATGCAAGTGAAGTTCTGGTGAATAGCAATATCAGACTGGTCTGG 135
Db      14441 CAAGAGCGTGATCAGCAAGCAAGAGCACTCTCTGATGAAAAAACATGGTCTTGTTTGG 14382

Qy      136  TCGTGGTCCAGCGCTTTATCAACCGGGGATGAAGCGGATGATTTGTTTCAGATCGGT 195
Db      14381 TCGTGGTTCAGCGCTTTTAAATAGGATATGAACGATGATTTGTTTCAAAATTGGC 14322

Qy      196  TGCATTGGCTTGGTCAAGGCGGTTGACAAAGTTCGATCTTTGGTACGATGTGAGATTTTCG 255
Db      14321 TGTATTGGATTGCTAAAAATCGGTTGATAAAATTTGATTTGTGATATGATGTGAAGTTTCG 14262

Qy      256  ACCTATGGGGTGGCAATGATCATCGGAGAAATTCAGCGCTTTTGGCGGATGACGGTACG 315
Db      14261 ACCTATGCTGTTCCAAATGATTAATGGTGAATCCAGCGATTCATTCCGGATGATGGAACA 14202

Qy      316  GTTAAGGTGAGTGGATCGGTTGAAAGAAACAGGGAATAAGGTGGCGGATCAAGGATGAA 375
Db      14201 GTCAAAAGTCAGCGGCTCACTAAAGGAACTCGGAAATAAATCCGGCGGGCAAGATGAA 14142

Qy      376  TTGTACAGCAATATCGGCGTGGCGGCAAGTGGCAGAGTGGCAGAGTGGGAATC 435
Db      14141 TTGTCAAGTCTCATGGAAGAATGGGAGCGTCCAGGAAATAGCGAATATCTAGATATC 14082

Qy      436  ACGGCGGAGGAAGTGTCTTTGGGCAAGAGGCAAGGAGCGGCTTCTCCATCATGAG 495
Db      14081 ACACAGAGGATGTGGTCTCTCGGCAAGAGCGGTGGGAGCGGCTGTGGATTCATGAA 14022

Qy      496  ACGTTTTTGAAAAATGACGGGATCCATCACTGATCGATCAGATAGCGGATGAAGT 555
Db      14021 ACGTTTATGAAAAATGATGGGAGCGGATTCATTAAGTCTCAAAATTTGCTGATTCATCA 13962

Qy      556  GTGAACAAGTGGTTTGAGAAAAATGGCTTGAAGGAGCGGATCAGCAGGCTGAGCGAGCGT 615
Db      13961 GAAGAAAGATGGTTTGATAAAATCGGCTGAAAGAGCGGATCAAGGAATTAGAAGAAAG 13902

Qy      616  GAGCAGCTCATGTCTAAGTGGGCTATTACAAGGATCAGACAGTCTGAGGTAGCAGAG 675
Db      13901 GAAAAACTCATTTGTGACTTAAGGATATTAAAGAGCAAGCAAGTCTGAGGTAGCAGAG 13842

Qy      676  CGTCTAGGGAATTTGCAAGGTCCAGGTCTCGGTTCTGGAAAAAGGATATCTGCTAAAGATC 735
Db      13841 AGACTCGGCTTTTCAAGGATCAAGTCTCGGCGCTCGAAAAAGAAATTTTAAACAAATC 13782

Qy      736  AAGGACCAAAATTGAACA 752
Db      13781 CAAATGCAAAATGGATCA 13765

```

RESULT 8
 CP000557_23/c
 WPCOMMENT

Sequence split into 36 fragments LOCUS CP000557 Accession CP000557

Fragment	Name	Begin	End
CP000557_00		1	110000
CP000557_01		100001	210000

CP000557_02	200001	310000
CP000557_03	300001	410000
CP000557_04	400001	510000
CP000557_05	500001	610000
CP000557_06	600001	710000
CP000557_07	700001	810000
CP000557_08	800001	910000
CP000557_09	900001	1010000
CP000557_10	1000001	1110000
CP000557_11	1100001	1210000
CP000557_12	1200001	1310000
CP000557_13	1300001	1410000
CP000557_14	1400001	1510000
CP000557_15	1500001	1610000
CP000557_16	1600001	1710000
CP000557_17	1700001	1810000
CP000557_18	1800001	1910000
CP000557_19	1900001	2010000
CP000557_20	2000001	2110000
CP000557_21	2100001	2210000
CP000557_22	2200001	2310000
CP000557_23	2300001	2410000
CP000557_24	2400001	2510000
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CP000557_26	2600001	2710000
CP000557_27	2700001	2810000
CP000557_28	2800001	2910000
CP000557_29	2900001	3010000
CP000557_30	3000001	3110000
CP000557_31	3100001	3210000
CP000557_32	3200001	3310000
CP000557_33	3300001	3410000
CP000557_34	3400001	3510000
CP000557_35	3500001	3550319

Continuation (24 of 36) of CP000557 from base 2300001 (CP000557 *Geobacillus thermodeni*)

Query Match 46.8% Score 353.6; DB 14; Length 110000;
 Best Local Similarity 68.9% Pred. No. 1.2e-101;
 Matches 485; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

```

Qy      53  TGAAGATTGATAGCCAAAGAGCCAAAGCTGGCGATACGGATGCAAGTGAGCTTCTGGTGA 112
Db      58581 TGAAGAGGCTGATCGCGCGAGTCAGGAAGGGGAGCCAAAGAGCGCGGATGAAATATTG 58522

Qy      113 ATACCAATATCAGACTGGTCTGGTGGTGGTCCAGGGCTTTATCAACGGCGGGTATGAAG 172
Db      58521 AAAAAAATATGGGCTGGTCTGGTGGTGGTCCAGGGTTCTTAAATGGTGGCTATGAAG 58462

Qy      173  CGGATGATTGTGTTTCAGATCGGTTGCATTGGCTTGGTCAAGGGCGTTGACAAGTTGATC 232
Db      58461 CGGATGATTGTGTTTCAAAATGGGCTGCATCGGCTTGTTAAATCAGTGGATAGTTGACT 58402

Qy      233  TTTGGTACGATGTGAGATTTTGGACCTATGGGGTGGCAATGATCATCGAGAAATTCAC 292
Db      58401 TATGGTATGAGGTCAAGTTTGGAGGTACGGGTGGGGTGGGATGATCATCGGGGAGATTGAGC 58342

Qy      293  GCTTTTGGGGGATGAAGGATCGGTTAAGGTGAGTGGTGGTAAAAGAAACAGGGAATA 352
Db      58341 GATTTGCTGGGGATGAAGGATCGGTTAAGGTGAGTGGTGGTAAAAGAGATGGGGAATA 58282

Qy      353  AGGTGGGGGATCAAGGATGAATTGTACAAGCAATTCGGGGTGGGGGACAGTACAG 412
Db      58281 AAATCGGCAAGAGGAGGAGGAACTGTCAAGAGCGGGGGGGGGGAGATCAACG 58222

Qy      413  AAGTGGCAGAGCAGTGGGAATCAAGCGGAGGAGTGGTCTTTGGCAGAGGAGGAGCA 472
Db      58221 AAATCGGCAAGCATTGGTGGTTGGCGGAGGAGTGGTCTTGGCAGAGGAGGAGTTC 58162

Qy      473  GAGGGCTTCTGCTCATGATGAGAGCGGTTTTTGAATGAGGGGATCCATCAGACTGA 532

```

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Db      58161  CCTCGCGGGGTGATTCATGAACAGTGTATGAAACGACGCGCATTCGATCAAGCTGC 58102
Qy      593    TGATCAGATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAAATTGCGCTTGAAGGACG 592
Db      58101  TGATCAAATCGCGATGCTGACGAGGGTTCATGGTTTGAGAAAATTGCGCTTAAAAAAG 58042
Qy      593    CCATCAGCAGGCTGAGCGAGGCTGAGCAGCTCATGGTCTACCTGGCTATTACAAGGATC 652
Db      58041  CGATTGAACAGCTCGATGAGCGGAAAGGCTCATGGTCTATTGGGTATTACAAGACC 57982
Qy      653    AGACACAGTCTGAGGTAGCAGAGGCTAGGGAATTCGACGGTCCAGGTCTCGGCTCTGG 712
Db      57981  AAAACAGTCCGAAGTGGCAGCAAGACTCGGCATCTCTCAAGTGCAAGTATCCCGGCTGG 57922
Qy      713    AAAAGCGTATCTGCTAACGATCAAGGAGCAAAATTGAACATTAG 756
Db      57921  AAAAGAAAATATTGCAGCACATAAAGGAAAAAATGGATGGTAG 57878

```

RESULT 9

AP006627_19

WPCOMMENT

Sequence split into 43 fragments LOCUS AP006627 Accession AP006627

Fragment Name	Begin	End
AP006627_00	1	110000
AP006627_01	100001	210000
AP006627_02	200001	310000
AP006627_03	300001	410000
AP006627_04	400001	510000
AP006627_05	500001	610000
AP006627_06	600001	710000
AP006627_07	700001	810000
AP006627_08	800001	910000
AP006627_09	900001	1010000
AP006627_10	1000001	1110000
AP006627_11	1100001	1210000
AP006627_12	1200001	1310000
AP006627_13	1300001	1410000
AP006627_14	1400001	1510000
AP006627_15	1500001	1610000
AP006627_16	1600001	1710000
AP006627_17	1700001	1810000
AP006627_18	1800001	1910000
AP006627_19	1900001	2010000
AP006627_20	2000001	2110000
AP006627_21	2100001	2210000
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AP006627_30	3000001	3110000
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AP006627_32	3200001	3310000
AP006627_33	3300001	3410000
AP006627_34	3400001	3510000
AP006627_35	3500001	3610000
AP006627_36	3600001	3710000
AP006627_37	3700001	3810000
AP006627_38	3800001	3910000
AP006627_39	3900001	4010000
AP006627_40	4000001	4110000
AP006627_41	4100001	4210000
AP006627_42	4200001	4303871

Continuation (20 of 43) of AP006627 from base 1900001 (AP006627 Bacillus clausii KSM)

Query Match 46.1% Score 348.4; DB 14; Length 110000;
 Best Local Similarity 68.2% Pred. No. 5.6e-100;
 Matches 484; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

```

Qy      37  CTGACCAATGACCAAGTGAAGATTGATAGCCAAAGAGCCAGCTGCGGATAOAGATGCA 96
Db      12188 CTATCCGATAAACAAGTGAAGAGCTGATTGCAAAAAGCCAGGAGCGACACAGAACCA 12247
Qy      97  CGTGAGCTTCTGTGAATAGCAATATCAGACTGGTCTGGTGGTGGTCCAGCGCTTTATC 156
Db      12248 CGGGATTGATGTGTAACCATTAACACAGCTCTGTCTGGTGGTGGTCCAGGTTTTTTG 12307
Qy      157  AAOCGGGGTATGAAGGGATGATTGTGTTTTCAGATGGGTCATTGGCTTCTCAAGGCC 216
Db      12308 AATOGGGGTTATGAGGACAGACCTTTTTCAAATTGGCTGATTGGTTTATTAAAGTCT 12367
Qy      217  GTTGACAAGTGTGATCTTTTGTACGATGTGAGATTTTGCACCTATGGGTCGCAATGATC 276
Db      12368 GTGCAAAATTTGAOCTTTCTATGATGTGAAATTTCTCAAGTATGCTGTGCAATGATT 12427
Qy      277  ATGGGAGAAATTCAGCGCTTTTTTGGGGATGAOGGTACGGTTAAGTCACTGATGATGTTA 336
Db      12428 ATTGGGAAATCCAAAGTTTTTTGGGGATGATGGTACGGTGAAGTGAAGCGGTCATT 12487
Qy      337  AAAGAAACAGGGAATGAAGTGGGGGATCAAGGATGAATTGTACAAGCAATTCGGCGGT 396
Db      12488 AAAGAAATTAAGCAATAAAATTTGCAAAAGCAAAAGAGAGCTGAOAGAAAGCTGGCGGG 12547
Qy      397  GCGGGCAAGTGTGACAGAGTGGCAGAGAGCTGGGAATCAAGCGGAGGAGTGTCTTT 456
Db      12548 GCGGGCAOCTTAATGAGATTGGGAACATTAGGGGTGAOCCCTGAGGAAATTTGATTT 12607
Qy      457  GCGCAAGAGGCAAGCAGAGCGCTTCTGATCATGAGAGGTTTTTGAAGTGAAGGC 516
Db      12608 GCTGGAGATGCCAAOAGGCTTTGTCTCAATCATGAAAGGCTCTATGAAGTATGATGC 12667
Qy      517  GATCCATCACACTGATGATCAGATAGGGATGAAGTGTGAACAAGTGGTTTGAGAAA 576
Db      12668 GAOCGATTAACACTGCTAGATCAAAATTTGGGAOCCACTCACAAGTCAAGTGGTTTGACAG 12727
Qy      577  ATTGCTTTGAAGGAGGCCATCAGCAGGCTGAGGGAGGCTGAGCAGCTCATGCTCATCTG 636
Db      12728 ATTGCTTTGAAGGAGGCCATTTGGAGCTTTGGGAAAGGGAGGGCTGATAGTATACTTG 12787
Qy      637  CGCTATTACAAGGATCAGACACAGTCTGAGGTAGCAGAGGCTGAGGATTTTGGCAGTTC 696
Db      12788 CGTTATTATAGGATCAACACAAATCAGAAGTGGCTGAAGGCTGAGGATTTTGGCAAGTG 12847
Qy      697  CAGGTCTCGGGTCTGAAAAAGGTATCCTGCTAAGCATCAAGGAGCAAT 746
Db      12848 CAGGTCTCTGGCTAGAGAAAAAATATTGGACAAATGAAGGAGCAAT 12897

```

RESULT 10

BACSPC2A

LOCUS

DEFINITION

BACSPC2A 864 bp DNA linear BCT 26-APR-1993
 B. subtilis spoliA gene encoding a sporulation-specific sigma factor, complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

M15744

M15744.1 G:143610

sporulation-specific sigma factor.

Bacillus subtilis

Bacillus subtilis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 864)

Yudkin, M.D.

REFERENCE

AUTHORS

TITLE

Structure and function in a *Bacillus subtilis* sporulation-specific sigma factor: molecular nature of mutations in spoliA

JOURNAL J. Gen. Microbiol. 133 (Pt 3), 475-481 (1987)
 PUBMED 3116160
 COMMENT Original source text: B. subtilis (strain 168) DNA, clone BglII/PstI.
 Draft entry and clean copy sequence for [1] kindly provided by M.D. Yukin, 26-MAY-1987.

FEATURES
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 90..857
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 DDGTVKVSRLKELONKIPRAKDELKTLGRVPTVCEIADHLEI EAEDVLAQEA
 PSSIHETVYENDGPI TLLDQADNSEEKWFDKIALKEALSDLEEREKLI VYLRYK
 QTCSEVAERLIGSQVQSRLEKLIKQIKVMDHTDQ"
 CDS
 1..864
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 DDGTVKVSRLKELONKIPRAKDELKTLGRVPTVCEIADHLEI EAEDVLAQEA
 PSSIHETVYENDGPI TLLDQADNSEEKWFDKIALKEALSDLEEREKLI VYLRYK
 QTCSEVAERLIGSQVQSRLEKLIKQIKVMDHTDQ"
 ORIGIN 2 bp upstream of ClaI site.

Query Match 45.7% Score 345.6; DB 14; Length 864;
 Best Local Similarity 68.5% Pred. No. 2.1e-99;
 Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

Qy 10 GATATCAAAAAAGGAGTCAACCATTTCTGACCAATGAACAGTGAAAGATTTGATAGCC 69
 Db 102 GTTAAGAAAAAGGCAAAAAAGCTCAGCTGAAGGATCATGAAGTAAAGGATTAATCAAA 161

Qy 70 AAGAGCCAAAGCTGGGATACGGATGCAAGTGAGCTTCTGGTGAATGCAATATCAGACTG 129
 Db 162 CAAAGCCAAAGTGGGATACGGATGCAAGTGAGCTTCTGGTGAATGCAATATCAGACTG 221

Qy 130 GTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 189
 Db 222 GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 281

Qy 190 ATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 249
 Db 282 ATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 341

Qy 250 TTTTCAAGCTATGGGATGCAATGATCATGAGAGAAATCAAGGCTTTTGGGATGAC 309
 Db 342 TTTTCAAGCTATGGGATGCAATGATCATGAGAGAAATCAAGGCTTTTGGGATGAC 401

Qy 310 GGTACGGTTAAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 369
 Db 402 GGTACGGTTAAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 461

Qy 370 GATGAATGTGCAAGCAATTCGGGCTGGGGCAAGATGCAAGGTGGCAAGAGCAGTG 429
 Db 462 GATGAATGTGCAAGCAATTCGGGCTGGGGCAAGATGCAAGGTGGCAAGAGCAGTG 521

Qy 430 GGAATCAAGCGGAGGAGAGTGTCTTGGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489
 Db 522 GGAATCAAGCGGAGGAGAGTGTCTTGGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 581

Qy 490 CATGAGAGCGTTTGGAAATGAGCGGATCCATCACACTGATGATCAGATAGCGAT 549
 Db 582 CATGAGAGCGTTTGGAAATGAGCGGATCCATCACACTGATGATCAGATAGCGAT 641

Qy 550 GAAGGTGTGAACAGTGGTTTGAAGAAATGGCTTGAAGAGCGCATCAGCAGGCTGAGC 609
 Db 642 GAAGGTGTGAACAGTGGTTTGAAGAAATGGCTTGAAGAGCGCATCAGCAGGCTGAGC 701

Qy 610 GAGGGTACGAGCTCATGCTACCTGGGCTATTACAAGGATCAGACACAGTCTGAGGTA 669
 Db 702 GAAAGGAAAAAACTAATGCTCTATCTCAGATATTATAAGACACACAGTCCGAGGTG 761
 Qy 670 GCAGAGGGTCTAGGGATTTCGAGGTCAGGTCCTGGGCTCTGAAAAAGGATATCTCGCTA 729
 Db 762 GCTGAGGGCTCTGGGATCTCTCAGGTCAGGTTCCAGGCTTAAAAAGAAATATTAATA 821
 Qy 730 ACGATCAAGAGCAAAATTGAACAT 753
 Db 822 CAGATCAAGGTTCAATGGATCAT 845

RESULT 11
 Z99116/c

LOCUS Z99116 204537 bp DNA linear BCT 18-APR-2005
 DEFINITION *Bacillus subtilis* complete genome (section 13 of 21): from 2409151 to 2613687.

ACCESSION Z99116 AL009126

VERSION Z99116.2 G:32468787

KEYWORDS

SOURCE *Bacillus subtilis* subsp. *subtilis* str. 168
 ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 168
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 204537)

AUTHORS

Kunst, F., Ogasawara, N., Mbszer, I., Albertini, A.M., Aloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Funa, S., Galizzi, A., Galleron, N., Ghim, S.Y., Gasser, P., Goffeau, A., Gollightly, E.J., Grandi, G., Guiseppe, G., Guy, B.J., Haga, K., Haech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hsiono, S., Hullo, M.F., Itaya, M., Jones, J., Joris, B., Karamata, D., Kasahara, Y., Kjaer, Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Konigstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Melado, R.P., Mizuno, M., Mestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portet, D., Porwollik, S., Prescott, A.M., Prescan, E., Puig, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadai, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scofield, F., Sekiguchi, J., Sekowska, A., Serr, S.J., Serr, P., Shi, B., Sol do, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tanakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vanni, F., Vassarotti, A., Vial, A., Vrbut, R., Weder, E., Weder, E., Weizenegger, T., Winters, P., Wpat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H.F., Zumbstein, E., Yoshikawa, H. and Danchi, N.

TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*

JOURNAL *Nature* 390 (6657), 249-256 (1997)

PUBMED 9384377

REFERENCE 2 (bases 1 to 204537)

AUTHORS Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchi, N.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-2003) I. Mbszer, A. Danchi, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: mbszer@pasteur.fr, adanchi@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48

COMMENT On Jul 7, 2003 this sequence version replaced gi:2634723.

This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at <http://genolist.pasteur.fr/SubtiList/>.

FEATURES	Location/Qualifiers
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CDS	/locus_tag="BSL23060" complement(739..903) /gene="ypzE" /locus_tag="BSL23060" /function="unknown" /codon_start=1 /translation="1" /protein_id="CAB14238.1" /db_xref="GI:2634741" /db_xref="SubtiList:BG13767" /db_xref="UniProtKB/Swiss-Prot:C82010" /translation="MKFPTGGDEPWALSPRAVFTAGFGEI PEPTVCSGNEKMEVHKRF EIEFFKRFFA"
gene	1130..2707 /gene="serA"
CDS	/locus_tag="BSL23070" 1130..2707 /gene="serA" /locus_tag="BSL23070" /EC_number="1.1.1.95" /function="serine biosynthesis" /codon_start=1 /translation="1" /product="phosphoglycerate dehydratase" /protein_id="CAB14239.1" /db_xref="GI:2634742" /db_xref="GOA:P35136" /db_xref="InterPro:IPR002912" /db_xref="InterPro:IPR006139" /db_xref="InterPro:IPR006140" /db_xref="InterPro:IPR006236" /db_xref="SubtiList:BG10509" /db_xref="UniProtKB/Swiss-Prot:P35136" /translation="MFRVLVSDKMSNDLQPLIESDFI EIVQKNVADAEDLHTFDAL LVRSATKVTEDLFNKMISLKI VGRAGVGDNI DEATKHGI VIANPNGNTI STAEH TFAM SSLMFI PQANI SVKSREVNRTAYVGSLEYGKTLG VGLGI GSEI AQRIAGF GMIVHVPDPFL TEERAKKI GVNRSITFEVLESADI ITVHTPLTKETKGLLNKTI AKT KKGVRLI NCARGI I DEALL EALENGHAGALDVFEVEPPVDNKLVDHPLVI ATPH LGASTKEAQLNVAQVSEEVLFQAKGLPVMISAI NLPAMTKDEFKPI KPYHQI AGKI GS

	<p>LVSCQMKEPVQDVAI QYEGTI AKLETSEI TKALLSGFLKPRVDSTVNEVNAAGWAKER GI SFSEKI SSSSESGYDNI SVKVTGDRSTFTVTATYI PHFGERI VEI NGFNI DFYPTG HLVYI QHDDTTGM GRVGRH LGDNDI NI ATMGVGRKEKGGEAI MMLSFDRHLEDKI VK ELTNVPI DI VSKVLI DLP"</p>
gene	<p>complement (2750..3517) /gene="ar oC" /locus_tag="BSL23080"</p>
CDS	<p>complement (2750..3517) /gene="ar oC" /locus_tag="BSL23080" /EC_number="4.2.1.10" /function="shikimate pathway" /codon_start=1 /transl_table=11 /product="3-dehydroquinate dehydratase" /protein_id="CAB14240.1" /db_xref="GI:2634743" /db_xref="GOA:P35146" /db_xref="InterPro:IPR001381" /db_xref="Subtilist:BG10538" /db_xref="UniProtKB/Swiss-Prot:P35146" /translation="MVLTI KGVSIGGVPII I PLMGKTEKI LNEAEAVKLLNPD VEAFVDFVEKANDREAVTKLI SKLRKSL EDKLF LFTFRTHKEGSGMEVDESSYLLLE SIA QTKDI DLI DI ELFGDANKALVSLAEENNVVYVMSNHFDEKTPVKDEI I SRLRK MDLGAH PKVAVMPNDTGDLTL LLDATYTKTI YADRP I I TMSMAATQLI SRLSGEV FGSACTFGAGEASAPGI PVSELRSLDI LHKNTRG"</p>
gene	<p>complement (3629..4735) /gene="rsi X"</p>
CDS	<p>/locus_tag="BSL23090" complement (3629..4735) /gene="rsi X" /locus_tag="BSL23090" /function="negative regulation of sigma-X activity" /notes="alternate gene name: ypuN" /codon_start=1 /transl_table=11 /protein_id="CAB14241.1" /db_xref="GI:2634744" /db_xref="GOA:P35166" /db_xref="Subtilist:BG10537" /db_xref="UniProtKB/Swiss-Prot:P35166" /translation="MKSEVNEEQI KELLSQLPAVKDHRSPQDI YKRLTMAKRINKPA VRW GPACAAAI AVYI AFI I SPHFDDAQPCKEASQENAVTKTETEDSPKAASSLDQ TSFVVPEKEQDNI TVAVADADTSI I PVSI QKTNADQI QDMFESSELGI LDHAI T I PTFI DEVEI KEKPKOKELSI RVHQPATFESI KDDTLIKLLKESLKWSPYKVKFSL DQNTGVRI GSYGTTFTEI SI PKOSKPSYLYQNKQGDFLVPSNHSFDTVKEAI KEME SSQEDITPLI QAGAVQSVTKKIKILYMFSSKESEVDDSI AGI LMEGLLLTAKEFG TEVFTETRTKKI GKYDI SDAI PVPAAPNPI SLN"</p>
gene	<p>complement (4671..5255) /gene="sigX"</p>
CDS	<p>/locus_tag="BSL23100" complement (4671..5255) /gene="sigX" /locus_tag="BSL23100" /function="may participate in the regulation of peptidoglycan synthesis and turnover" /notes="alternate gene name: ypuM" /codon_start=1 /transl_table=11 /product="RNA polymerase ECF (extracytoplasmic function)-type sigma factor (sigma-X)" /protein_id="CAB14242.1" /db_xref="GI:2634745" /db_xref="GOA:P35165" /db_xref="InterPro:IPR000838" /db_xref="InterPro:IPR007627" /db_xref="InterPro:IPR007630" /db_xref="InterPro:IPR013324" /db_xref="InterPro:IPR013325"</p>

gene

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 /db_xref="UniProtKB/Swiss-Prot:P35165"
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 YHTEFGSSEKTLWLSI ARHVAI DWFRKQQT RORI LGTFDWDTDQVRDQQLPDELA
 VQHNREI SCALDQCTI DORAVI LRFI GQYSI QETAKAL RFSESKVKTTQHRGLKV
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 complement (5459..7228)
 /gene="resE"
 /locus_tag="BSL23110"

Query Match 45.7% Score 345.6; DB 14; Length 204537;
 Best Local Similarity 66.5% Pred. No. 4,9e-99;
 Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

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Qy	70	AAGAGCAAGCTGGGATACGGATGCACTGAGCTTCTGTAATAGCAATATCAGACTG	129
Db	34163	CAAAAGCAAAAATGGGACCAAGCAAGAGCACTCTCATAGAAAAAACATGGCTCTT	34104
Qy	130	GTCGTGGTGGTGGTCAAGGGCTTTTATCAAGCGGGGTATGAAGGGGATGATTTGTTT	189
Db	34103	GTTTGGTCTGTGGTACAGGGCTTTTAAACAGAGGATATGAGCGTGAAGATCTCTT	34044
Qy	190	ATGGTGGTGGTGGTGGTCAAGGGCTTGAAGGTGGATCTTCTGTAAGATGTGAGA	249
Db	34043	ATGGTGGTGGTGGTGGTCAAGGTGGATCTTGAAGGTGGATCTTGAAGGTGGAT	33984
Qy	250	TTTTCAAGCTATGGGGTGGCAATGATCATGCGAAGAAATCAAGCGCTTTTGGGG	309
Db	33983	TTTTCAAGCTATGGGGTGGCAATGATCATGCGAAGAAATCAAGCGCTTTTGGGG	33924
Qy	310	GGTACGGTTAAGGTGAGTGGATGGTAAAAAGAAACAGCGAATAAGGTGGGGGAT	369
Db	33923	GGAAAGTAAAGGTATCAAGGTGATTAAGAAAGGCTTGAAGAAAGAAATCGGGG	33864
Qy	370	GATGAATTTGTAAGCAATTTGGGGGTGGGGGCAAGTGGCAAGTGGCAAGCAGTG	429
Db	33863	GATGAGCTTTGAAAAACTGGGCAAGTGGGGGCAAGTGGCAAGTGGCAAGCAGTG	33804
Qy	430	GGAATCAAGCGGAGGAAGTGTCTTTGGGCAAGAGGCAAGCAGCGCTTCTCCATC	489
Db	33803	GAGATTGAAGCTGAGGATGTTGTACTGGGGCAAGAGGCGGTAAAGGCTTCTCTG	33744
Qy	490	CATGAGCGGTTTTTAAAAATGAAGCGGATCCATCAGCTGATGATCAGATAGCGAT	549
Db	33743	CAAGAAAGGTTTTTAAAAATGAAGCGGATCCATCAGCTGATGATCAGATAGCGAT	33684
Qy	550	GAAGGTGTGAACAAAGTGGTTTGAAGAAATGGCTTGAAGAAAGCGATCAGCAGG	609
Db	33683	AACTCAGAGAAAGAAATGGTTTGAAGAAATGGCTTGAAGAAAGCGATCAGCAGG	33624
Qy	610	GAGGTGAGCAGCTCATGCTCACTGGGCTATTACAAGGATCAGACACAGTCTGAGTA	669
Db	33623	GAAGGGGAAAAAATAAGTGTCTATCTCAGATATTATTAAGACAGACACAGTCTG	33564
Qy	670	GCAGAGGTCTAGGGATTTGGCAGGTCCAGGTCTGGGCTCTGAAAAAGGATATCTG	729
Db	33563	GCTGAGGGCTGGGGATCTCTCAGGTGAGGTTCGAGGCTTGAAGAAAGAAATATT	33504
Qy	730	ACGATCAAGGAGCAAAATTAACAT	753
Db	33503	CAGTCAAGGTTCAAAATGGATCAT	33480

RESULT 12
 BACJH642

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 YKPVGL YVEGDLVGFAMVGL FPEYEDNKNKGVWLD RFFI DERYGQGL GKGM KALI
 QHLAEL YKOKRI YLSI FENNI HAI RLYQRFQFQNGELDFNGEKVMKEL"
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 G RMPFFFAAI ALI AAVTSVFI LKESLSI EERHQLSSHTKESNFI KDLKRSI HPVYF
 I AFI I FVMAFGL SAYETVFSLSFDHKFGFTPKDI AAI I TISI VAVVI QVLLFGKLV
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 2757. . 3578
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 VQCYELDEGYPI GG FAREQ LEKDFYNYSFYI KVKGDAENI NYHVRPKQL YAVGYE
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 I VDI"
 4108. . 4111
 4120. . 4680
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 / translation = 1
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 / translation = "MAYNPFSPQCYVYVTPVMNDGRSVYVVI PNEMEKVHRGADLRS
 SYEDRN LLLKDYGPKEFVNI NRATKQNTFTFALWKGKHFQVTLMSLG GEDI GLEI
 HFNVDQFLRI EQQGI VKMGSKDHLNFGRNYYDSAI VVPGATVHNI NTGNTPLKL
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 5458. . 5464
 5473. . 5664
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 / db_xref = "GI:1303703"
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 5797. . 5801
 5809. . 6291


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GFNALKEELI PVKKGFLKMFQGMMPGADKMG SKMNFAGVGPKM KNVMKKGNVL
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6477. .7034
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ESLNI LDVREI EYEYKAHI PGVH PLGEVEKRANELNENDEI YI I CHSGRRSEMAAR
TKMGQFKKVI NVVPGMRDWTGKE"
7361. .7367
7376. .7486
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7615. .8502
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VI AEKTKATYWLPLFKDI DSEVEFYDQPLNEGDI I GNNTI KI QPI YSPG-TI GSTSF
YDDOYLLSGDI LPFI DSI GRPDLAGMADWWGDLRKTLYSRYKALKDIL VLPPIHFI I
DELNENSGVGKGLTFSFENHGLNI ADETEFRHLVTDHLPFGPNAYQEI RETNMGI S
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8536. .8763
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/ db_xref = "G : 1303708"
/ translation = "MKSDKVLDAKGLACPMPI VRTTKAMNELESQI LEVHATDKGAK
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8807. .8815
8824. .9609
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/ prote_n_id = "BAA12365.1"
/ db_xref = "G : 1303709"
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I SEKG NFI YGI LAI I AVI LMFI PKGQKGQEHSEDKEVI FNKVLASSAFI I GGVS
I LGAGGAFI LVPI MLSI LNI PVRVTVAASSLAITFSSI GATVGKVI TQGVLFVFLV
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10177. .10182

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Query Match 45.7% Score 345.6; DB 14; Length 282700;
Best Local Similarity 66.5% Pred. No. 5.2e-99;
Matches 495; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

Qy 10 GATATCAAAATGCGAGTCAACATTTCTGACCAATGACCAAGTAAAAGATTTGATAGCC 69

RESULT 13
BA000004_16
WPCOMMENT

Sequence split into 42 fragments LOCUS BA000004 Accession BA000004

Fragment	Name	Begin	End
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BA000004	03	300001	410000
BA000004	04	400001	510000
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BA000004	06	600001	710000
BA000004	07	700001	810000
BA000004	08	800001	910000
BA000004	09	900001	1010000
BA000004	10	1000001	1110000
BA000004	11	1100001	1210000
BA000004	12	1200001	1310000

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BA000004_14	1400001	1510000
BA000004_15	1500001	1610000
BA000004_16	1600001	1710000
BA000004_17	1700001	1810000
BA000004_18	1800001	1910000
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BA000004_36	3600001	3710000
BA000004_37	3700001	3810000
BA000004_38	3800001	3910000
BA000004_39	3900001	4010000
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BA000004_41	4100001	4202352

Continuation (17 of 42) of BA000004 from base 1600001 (BA000004 *Bacillus halodurans* C

Query Match 45.4% Score 343; DB 14; Length 110000;
 Best Local Similarity 67.3% Pred. No. 3.1e-98;
 Matches 484; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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Qy	98	GTGAGCTTCTCGTGAATAGCAATATCAGACTGGTCTGGTCCGTGGTCCAGCGCTTTATCA	157
Db	14427	GAGATCAAATCGTCAGTGTGAACACTGGCTCGTATGGTCTGTGTGCAACGATTCCTAA	14486
Qy	158	ACCGCGGGTATGAAGCGGATGATTTGTTTCAGATCGGTTGCATTGGCTTGCTCAAGCGCG	217
Db	14487	ATCGCGGGTATGAAGCAGACGACCTGTTTCAAATTTGGTTCGATTGGCTTGATTAATCAG	14546
Qy	218	TTGACAAGTTGATCTTTTGTGAAGATGTGAGATTTTTCGACCTATGGCGTGCACATGATCA	277
Db	14547	TGATAAATTCGATTTTGTGTGAAGATGTCAAGTTTTCGACCTATGGCGTGCACATGATCA	14606
Qy	278	TCGCAAAATTCACGCTTTTTCGCGGATGACGGTACGGTAAAGGTCAGTGCATCGTTAA	337
Db	14607	TCGCTGAATCCACGATTCCTTCGCGATGATGGTACGGTAAAGGTAAGTGGCTGCATTAA	14666
Qy	338	AAGAAACAGCGAATAGCGTGGCGGATCAAGGATGAATTTGTACAAGCAATTGGCGCGTG	397
Db	14667	AGGAGCTTGGCAATAAATTCGGAAGCTCAAGGATGATATGAAGAGACGCTGGGTGGGA	14726
Qy	398	CCCCACGATCGCAGAAGTGGCAGAAGCAGTGGCAATCACCGCGGAGGAAGTAGTCTTTG	457
Db	14727	CGCGACGGTGAATGAATTCGGGAGCAGTAGAAATTAAGCCAGGAAGTGGTCTTTG	14786
Qy	458	CGCAAGAGCGAAGCAGAGCGCTTCTTCATCCATGAGACCGTTTTTGAATTAAGCGCG	517
Db	14787	CGCGGATTCGAAGTGGCTGGCTAAGTTCCATCCATGAGACTGTCTATGAATTAAGCGCG	14846
Qy	518	ATCCATCAGCTGATCGATCAGATAGCGGATGAAGGTGTGAACAAGTGGTTTGAGAAA	577

RESULT 14
CP000764_28/ c
WPCOMMENT

Sequence split into 41 fragments LOCUS CP000764 Accession CP000764

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CP000764	02	200001	310000
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Continuation (29 of 41) of CP000764 from base 2800001 (CP000764 *Bacillus cereus* subsp.

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Qy 467 CAAGCAGAGCGGCTTCTCATCATGAGACGGTTTTTGAAATGAGCGGATCGCATCA 526

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Qy 587 AGGAGCGCATCAGGAGCGTGAAGCGGATGAGCAGCTCATGCTCACTGGCGATTACCA 646

Db 53239 AAGAAGCAATAAGAGAAGTATGATGAGCGGAAAGCGTTAATGTATATTGGCGATTATA 53180

Qy 647 AGGATCAGACACAGTCTGAGGTAGCAGAGCGTCTAGGATTTGGCAGGTCCAGTCTGGC 706

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RESULT 15

X63757

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

X63757

1920 bp

DNA

linear

BCT 18-APR-2005

B. megaterium genes spoIIA, spoIIB, spoIIC, pbp and spoVA.

X63757.1 S46395

X63757.1 G:39650

pbp gene; spoIIA gene; spoIIB gene; spoIIC gene; spoVA gene.

Bacillus megaterium

Bacillus megaterium

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1

Tao, Y. P., Hudspeth, D. S. and Vary, P. S.

Cloning and sequencing of the Bacillus megaterium spoIIA operon

Biochimie 74 (7-8), 695-704 (1992)

1391049

2 (bases 1 to 1920)

Vary, P. S.

Direct Submission

Submitted (02-JAN-1992) P. S. Vary, Northern Illinois University,

Dept. of Biological Sciences, DeKalb, Illinois 60115-2861, USA

On Jun 23, 2005 this sequence version replaced gi:258183.

Location/Qualifiers

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SCORE 3.0